

Cluster tool instructions

This tool can be used to:

- Perform Cluster analysis.
- Visualize clusters using a tree plot (dendrogram).
- Highlight important clusters.

Instructions:

1) Prepare dataset in the following format.

Column 1: unique IDs
(no spaces or hyphens)

Columns with one or more
linguistic variables
(relative frequencies)

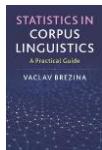
	A	B	C	D	E	F	G	H	I	K	L	
1	ID	PAST	PERF	PRES	PLACE	TIME	1PRON	2PRON	3PRON	IT	DEMPRON	INDPRON
2	S_dialogue_priv	5.0752	0.3505	8.9916	0.2738	0.4968	5.423	2.7447	4.2475	2.6959	0.888	0.0473
3	S_dialogue_pub	3.406625	0.511	8.287375	0.283125	0.53875	4.061	2.366875	2.54125	2.07675	1.0015	0.045875
4	S_monologue_priv	2.767143	0.448571	7.509429	0.498	0.762571	2.689	1.793857	2.537714	1.965	0.816143	0.034143
5	S_monologue_scripted	0.156	0.7286	5.9382	0.4424	0.7078	1.4026	0.4792	2.3212	1.1802	0.4058	0.0256
6	W_student_writing	3.008	0.2529	5.146471	0.238235	0.375294	0.788824	0.144706	2.692353	1.097647	0.653529	0.030588
7	W_letters						5.9394	4.375455	1.599697	1.476364	1.048788	0.383636
8	W_academic						0.3365	0.51125	0.06425	0.9335	0.7785	0.3975
9	W_popular						0.56875	0.5755	0.11025	1.53675	0.99225	0.3205
10	W_reportage						0.731	0.5055	0.089	2.1685	0.997	0.2275
11	W_instructions						0.2655	0.6205	1.6925	1.0135	0.831	0.449
12	W_persuasive						1.897	1.152	5.309	0.256	0.376	0.075
13	W_creative						8.416	0.7715	3.9185	0.6725	0.478	2.8785
14												

2) Copy and Paste the data into the Cluster tool.

Correlation calculator Clusters MD analysis Videos

1. Paste tab delimited data including header row and id column. For help click [here](#).

ID	PAST	PERF	PRES	PLACE	TIME	1PRON	2PRON	3PRON	IT	DEMPRON	INDPRON	DO	NOMZ	NN
PASS	BYPASS	BE	EXIST	CAUS	COND	OSUB	PP	JJATR	PRIV	ADV	TTR	MWL	CONT	
CONJ	DWNT	HDG	AMP	EMPH	DEMO	POSS	PRED	PUBV		SUAV	SMAP			
SYNEG	ANNEG													
S_dialogue_priv	5.0752	0.3505	8.9916	0.2738	0.4968	5.423	2.7447	4.2475	2.6959	0.888	0.0473	0.4089		
0.3955	14.9268	0.56	0.0122	3.2432	0.4298	0.2339	0.1089	0.3518	0.1356	6.0483	5.0543	0.8469	5.4594	
164.21	3.7473	0.041	0.1693	0.2813	0.1667	1.815	1.351	0.6582	0.1716	0.9636	0.7357	3.0324	0.1711	
0.0408	5.0874	0.1822	1.8282											
S_dialogue_pub	3.406625	0.511	8.287375		0.283125		0.53875	4.061	2.366875			2.54125		
2.07675	1.0015	0.045875		0.320875		1.707375	16.34525	0.84025	0.0495	2.76075	0.480125			
0.267625		0.065125		0.458625		0.137375	8.426	5.1215	0.7165	4.817125		175.3375		
4.111125		0.087625		0.128	0.169875		0.33075	1.064875	1.8195	0.723625		0.174375		
0.83525	0.813625		2.234375		0.333625		0.085125	3.7435	0.165625		1.48525			
S_monologue_unscripted				2.767142857		0.448571429	7.509428571	0.498	0.762571429	2.689	1.793857143			



3) Select the appropriate options or leave the defaults.

2. Select parameters.

Transform data to z-scores

Useful if linguistic variables measured on different scales (default)

Distance measure: **Manhattan distance**

Clustering method: **Ward's method**

Different distance measures

3. Select highlight.

How many cluster groups do you want to highlight? **5**

Different amalgamation options

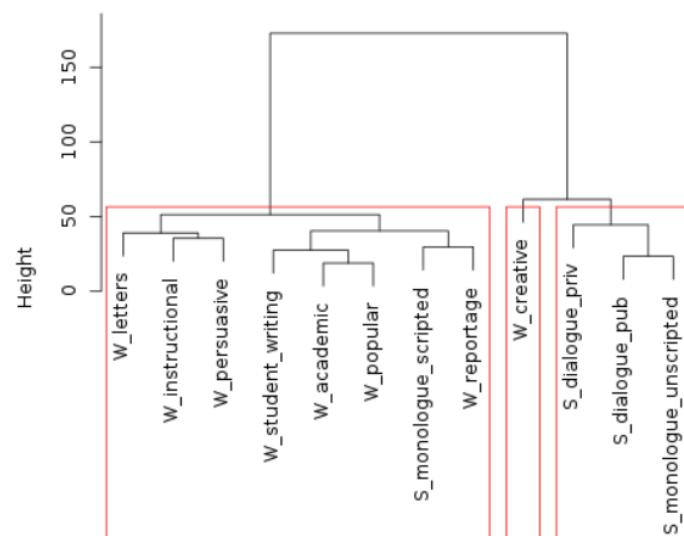
Option to highlight clusters in the output

4) Click 'Analyze'.

5) The output

Tree plot (dendrogram)

3 cluster groups were highlighted.



Read from the bottom.
Important clusters highlighted

- R R code that performs the analysis can be viewed and copied when going with the mouse pointer to [R code](#)